

# Sequence Listing

<110> Baker, Kevin P.  
 Botstein, David  
 Desnoyers, Luc  
 Eaton, Dan L.  
 Ferrara, Napoleone  
 Fong, Sherman  
 Gao, Wei-Qiang  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, Christopher J.  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Pan, James  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Smith, Victoria  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Watanabe, Colin K.  
 Williams, P. Mickey  
 Wood, William I.

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<210> 8
<211> 189
<212> PRT
<213> Homo sapiens

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<220>
<221> sig_peptide
<222> 1-24
<223> Signal Peptide

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<220>
<221> misc_feature
<222> 4-10, 5-11, 47-53, 170-176, 176-182
<223> N-Myristoylation Site.

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<220>
<221> misc_feature
<222> 44-85
<223> G-protein Coupled Receptors Proteins.

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<220>
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<222> 54-65
<223> Prokaryotic Mmembrane Lipoprotein Lipid Attachment Site.

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<220>
<221> misc_feature
<222> 82-86
<223> Casein Kinase II Phosphorylation Site.

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<221> TRANSMEM
<222> 86-103, 60-75
<223> Transmembrane Domain

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<222> 144-151
<223> Tyrosine Kinase Phosphorylation Site.

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Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His
  1              5              10              15

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 20 25 30  
 Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr  
 35 40 45  
 Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile  
 50 55 60  
 Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln  
 65 70 75  
 His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr  
 80 85 90  
 Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp  
 95 100 105  
 Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val  
 110 115 120  
 Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln  
 125 130 135  
 Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr  
 140 145 150  
 Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser  
 155 160 165  
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala  
 170 175 180  
 Gly Leu Ala Leu Glu Ile Arg Ser Leu  
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<210> 9  
 <211> 1508  
 <212> DNA  
 <213> Homo sapiens

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 ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200  
 tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250  
 aacttttgat aaaaagggat ttcatgtaat cgctgcctgt ctgactgaat 300  
 caggatcaac agctttaag gcagaaacct cagagagact tcgtactgtg 350  
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

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 aaaaaaaaa 1508

<210> 10  
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 <212> PRT  
 <213> Homo sapiens  
  
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 <222> 1-17  
 <223> Signal Peptide  
  
 <220>  
 <221> misc\_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212

<223> N-myristoylation Sites.

<220>

<221> misc\_feature

<222> 39-42

<223> Glycosaminoglycan Attachment Site.

<220>

<221> TRANSMEM

<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc\_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

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20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
125 130 135

Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
140 145 150

Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
155 160 165

Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys  
170 175 180

Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
185 190 195



Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
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Pro	Lys	Ala	Val											

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

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 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200  
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 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
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 gggttaaaac cagcaaattc acccgtctta ccagtcctc agaaggcgga 450  
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
          20          25          30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
          35          40          45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
          50          55          60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
          65          70          75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
          80          85          90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
          95          100          105

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Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu Ile	Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro Gln	Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser Gln	Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln Ile	Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu Ala	Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly Asp	Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu Pro	Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro Thr	Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val His	Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His Ala	Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu Lys	Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu Thr	Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg Lys	Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His Phe	Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg Ile	Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser Leu	Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro Ala	Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile Gly	Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr Val	Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

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Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
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Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
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His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
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<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-24  
<223> Synthetic construct.

<400> 14  
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<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-44  
<223> Synthetic construct.

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<210> 16  
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<212> DNA  
<213> Homo sapiens

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cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
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aaaaaaaaaa aaaaaaaaaa aaaa 1524

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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
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<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

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 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

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 <222> 154-158  
 <223> N-glycosylation site.

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 <223> Tyrosine kinase phosphorylation site.

<400> 17

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Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
 20 25 30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
 35 40 45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
 50 55 60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
 65 70 75

Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
 80 85 90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
 95 100 105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
 110 115 120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
 125 130 135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu



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Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp
				155					160					165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala
				170					175					180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His
				185					190					195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His
				200					205					210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly
				215					220					225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu
				230					235					240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe
				245					250					255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg
				260					265					270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly
				275					280					285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu
				290					295					300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp
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 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45  
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
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Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
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<212> DNA

<213> Homo sapiens

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ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150  
ggctccgggg cggcccgcta ggccagtgcg ccgcccgtcg cccgcaggc 200  
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tggtgtgcag cagcctggaa ctgcgcagc tcctgcccc agatactctg 450  
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<210> 24
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<223> Signal peptide.

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<222> 13-40
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Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
          35          40          45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
          50          55          60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
          65          70          75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
          80          85          90

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Asn	Lys	Ile	Ser	Glu 95	Leu	Lys	Asn	Gly	Ser 100	Phe	Ser	Gly	Leu	Ser 105
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Asp	Pro	Gly	Ala	Phe 125	Trp	Gly	Leu	Ser	Ser 130	Leu	Lys	Arg	Leu	Asp 135
Leu	Thr	Asn	Asn	Arg 140	Ile	Gly	Cys	Leu	Asn 145	Ala	Asp	Ile	Phe	Arg 150
Gly	Leu	Thr	Asn	Leu 155	Val	Arg	Leu	Asn	Leu 160	Ser	Gly	Asn	Leu	Phe 165
Ser	Ser	Leu	Ser	Gln 170	Gly	Thr	Phe	Asp	Tyr 175	Leu	Ala	Ser	Leu	Arg 180
Ser	Leu	Glu	Phe	Gln 185	Thr	Glu	Tyr	Leu	Leu 190	Cys	Asp	Cys	Asn	Ile 195
Leu	Trp	Met	His	Arg 200	Trp	Val	Lys	Glu	Lys 205	Asn	Ile	Thr	Val	Arg 210
Asp	Thr	Arg	Cys	Val 215	Tyr	Pro	Lys	Ser	Leu 220	Gln	Ala	Gln	Pro	Val 225
Thr	Gly	Val	Lys	Gln 230	Glu	Leu	Leu	Thr	Cys 235	Asp	Pro	Pro	Leu	Glu 240
Leu	Pro	Ser	Phe	Tyr 245	Met	Thr	Pro	Ser	His 250	Arg	Gln	Val	Val	Phe 255
Glu	Gly	Asp	Ser	Leu 260	Pro	Phe	Gln	Cys	Met 265	Ala	Ser	Tyr	Ile	Asp 270
Gln	Asp	Met	Gln	Val 275	Leu	Trp	Tyr	Gln	Asp 280	Gly	Arg	Ile	Val	Glu 285
Thr	Asp	Glu	Ser	Gln 290	Gly	Ile	Phe	Val	Glu 295	Lys	Asn	Met	Ile	His 300
Asn	Cys	Ser	Leu	Ile 305	Ala	Ser	Ala	Leu	Thr 310	Ile	Ser	Asn	Ile	Gln 315
Ala	Gly	Ser	Thr	Gly 320	Asn	Trp	Gly	Cys	His 325	Val	Gln	Thr	Lys	Arg 330
Gly	Asn	Asn	Thr	Arg 335	Thr	Val	Asp	Ile	Val 340	Val	Leu	Glu	Ser	Ser 345
Ala	Gln	Tyr	Cys	Pro 350	Pro	Glu	Arg	Val	Val 355	Asn	Asn	Lys	Gly	Asp 360
Phe	Arg	Trp	Pro	Arg 365	Thr	Leu	Ala	Gly	Ile 370	Thr	Ala	Tyr	Leu	Gln 375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro

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Gln Asp Glu Arg	Lys 395	Ala Trp Arg Arg	Cys 400	Asp Arg Gly Gly	Phe 405
Trp Ala Asp Asp	Asp 410	Tyr Ser Arg Cys	Gln 415	Tyr Ala Asn Asp	Val 420
Thr Arg Val Leu	Tyr 425	Met Phe Asn Gln	Met 430	Pro Leu Asn Leu	Thr 435
Asn Ala Val Ala	Thr 440	Ala Arg Gln Leu	Leu 445	Ala Tyr Thr Val	Glu 450
Ala Ala Asn Phe	Ser 455	Asp Lys Met Asp	Val 460	Ile Phe Val Ala	Glu 465
Met Ile Glu Lys	Phe 470	Gly Arg Phe Thr	Lys 475	Glu Glu Lys Ser	Lys 480
Glu Leu Gly Asp	Val 485	Met Val Asp Ile	Ala 490	Ser Asn Ile Met	Leu 495
Ala Asp Glu Arg	Val 500	Leu Trp Leu Ala	Gln 505	Arg Glu Ala Lys	Ala 510
Cys Ser Arg Ile	Val 515	Gln Cys Leu Gln	Arg 520	Ile Ala Thr Tyr	Arg 525
Leu Ala Gly Gly	Ala 530	His Val Tyr Ser	Thr 535	Tyr Ser Pro Asn	Ile 540
Ala Leu Glu Ala	Tyr 545	Val Ile Lys Ser	Thr 550	Gly Phe Thr Gly	Met 555
Thr Cys Thr Val	Phe 560	Gln Lys Val Ala	Ala 565	Ser Asp Arg Thr	Gly 570
Leu Ser Asp Tyr	Gly 575	Arg Arg Asp Pro	Glu 580	Gly Asn Leu Asp	Lys 585
Gln Leu Ser Phe	Lys 590	Cys Asn Val Ser	Asn 595	Thr Phe Ser Ser	Leu 600
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Ser

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 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
                   35                  40                  45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
                   50                  55                  60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
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 Lys Gly Ser Gln Lys Ser  
                   80

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 <212> DNA  
 <213> Homo sapiens

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<400> 31

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Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	
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Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	
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Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	
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Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	
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Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	
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His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	
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Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	
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Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	
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Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	
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Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
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Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
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Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
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Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
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Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
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35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
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Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp  
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
230 235 240

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Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
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Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
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Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
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Glu	Pro	Glu	Glu	Gln										
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<220>
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<223> Synthetic construct
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<210> 35
<211> 50
<212> DNA
<213> Artificial

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 <222> 1-23  
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 ggcgagccct aactatccag gag 23

<210> 38  
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<400> 38  
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<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 39  
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<210> 40  
 <211> 2084  
 <212> DNA  
 <213> Homo sapiens

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gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250  
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gcccaactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000
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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

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<400> 41

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          20          25          30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
          35          40          45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
          50          55          60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
          65          70          75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
          80          85          90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
          95          100          105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
          110          115          120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
          125          130          135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
          140          145          150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
          155          160          165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
          170          175          180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
          185          190          195

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Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
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Arg	Thr	Ser	Val											

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350  
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<210> 43  
<211> 263  
<212> PRT  
<213> Homo sapiens

<400> 43  
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20 25 30  
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
35 40 45  
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr	65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys	80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu	95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp	110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp	125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr	140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu	155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe	170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val	185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn	200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe	215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala	230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile	245	250	255
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<210> 44

<211> 24

<212> DNA

<213> Artificial

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<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

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<210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-20  
<223> Synthetic construct.

<400> 45  
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<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

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<222> 1-26  
<223> Synthetic construct.

<400> 46  
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<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgaac cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
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 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
 attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950  
 aaaaaaaaa aaaaaaaga 1969

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 <211> 283  
 <212> PRT  
 <213> Homo sapiens

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 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45  
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60  
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
 80 85 90  
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
 95 100 105  
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
 110 115 120  
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
 125 130 135  
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
 140 145 150  
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
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Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
				260					265					270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
				275					280					

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<210> 51
<211> 1734
<212> DNA
<213> Homo sapiens

<400> 51
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<210> 52  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

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Gly	Ala	Ala	Gly	Ser	65	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
				65						70					75
Arg	Glu	Ala	Val	Gly	80	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
				80						85					90
Ala	Ala	Asp	Ala	Leu	95	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95						100					105
Leu	Gly	Asn	Thr	Gly	110	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
				110						115					120
Ile	Arg	His	Gly	Ala	125	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
				125						130					135
Pro	Gly	His	Ser	Gly	140	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
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 agataagctg gcaagaggaa ggatcccagg cacatgggtc atcacgagca 4050  
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<210> 58  
 <211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
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Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
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Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
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His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
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His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
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Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
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Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
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Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
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Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
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Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
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Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
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Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu
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Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met
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Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr
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Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser
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Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu
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Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala
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Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala
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Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln
				380					385					390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln
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Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp
				410					415					420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu
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Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg
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Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu
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Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser
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Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro
				485					490					495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val
				500					505					510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile
				515					520					525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu
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Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys
				545					550					555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg



560										565				570			
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln			
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Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp			
				590					595					600			
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile			
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Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile			
				650					655					660			
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly			
				665					670					675			
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu			
				680					685					690			
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr			
				695					700					705			
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr			
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Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met			
				725					730					735			
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr			
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Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His			
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Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn			
				785					790					795			
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr			
				800					805					810			
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro			
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Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg			
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<211> 25
<212> DNA
<213> Artificial
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<220>  
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<222> 1-25  
<223> Synthetic construct.

<400> 59  
gggaaacaca gcagtcattg cctgc 25

<210> 60  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 60  
gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-42  
<223> Synthetic construct.

<400> 61  
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<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
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cacgggcccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgtc 150  
tgctgctcct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgcg 200  
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250  
cctcttcacc acgccgggtg tcccagcgc cctcactacc ccaggcctca 300  
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<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

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Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

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290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro	
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<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

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<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

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<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

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tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300

gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350

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<210> 68  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
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 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
 35 40 45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
 50 55 60



Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
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Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
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Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
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Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
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<210> 69

<211> 3170

<212> DNA

<213> Homo sapiens

<400> 69

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<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

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Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
          35             40             45

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Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
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Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
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His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
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Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
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Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
140 145 150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
170 175 180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
215 220 225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
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Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
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Cys Gln Lys Ile

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<211> 1809  
<212> DNA  
<213> Homo sapiens

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 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly	20	25	30	
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser	35	40	45	
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr	50	55	60	
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr	65	70	75	
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val	80	85	90	
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val	95	100	105	
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val	110	115	120	
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys	125	130	135	
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys	140	145	150	
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser	155	160	165	
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg	170	175	180	
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro	185	190	195	
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu	200	205	210	
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro	215	220	225	

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys  
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser  
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser  
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln  
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn  
305 310 315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr  
320 325 330

Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg  
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp  
350 355 360

Leu Ile Arg

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<211> 22  
<212> DNA  
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<400> 74  
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<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

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<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
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Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
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Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens

<400> 78

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<400> 79

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				20					25					30
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
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Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
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Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
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Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
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Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
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Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser	Ser
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	425	430	435
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr	Gly
	440	445	450
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Ala Cys Ser Thr	Leu Leu Val His Leu	Ile	
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 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
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 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
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 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
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 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
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Asp	Ile	Tyr	Gln	Met	Ala	Leu	Asn	Gln	Ala	Leu	Lys	Asp	Leu	Lys
				185					190					195
Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr
				200					205					210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala
				215					220					225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr
				230					235					240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp
				245					250					255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro
				260					265					270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala
				275					280					285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln
				290					295					300
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala
				305					310					315
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile
				320					325					330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg
				335					340					345
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg
				350					355					360
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn
				365					370					375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu
				380					385					390
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala
				395					400					405
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu
				410					415					420
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp
				425					430					435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser
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Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu

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515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

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 ccccctcgca gggctctgaat ttctgtctgc tgttcacaaa gatgcttttt 250  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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			20					25						30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			

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His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys	Val		
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Glu His Ala Tyr	Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser	Tyr		
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Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val	Val		
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile	Arg		
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Leu Leu Ala Asp	Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe	Pro		
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln	Asn		
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala	Val		
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys	Gly Ile Ile Arg His	Asp		
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Ser Phe Trp Asp	Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser	Leu		
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Gly Gly Arg Val	Arg Val Ile Val Thr	Gly Ala Ala Pro Met	Ser		
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Thr Ser Val Met	Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln	Val		
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Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr	Phe		
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly	His Val Gly Val Pro	Leu		
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp	Val Ala Asp Met Asn	Tyr		
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Phe Thr Val Asn	Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr	Asn		
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Val Phe Lys Gly	Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu	Ala		
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Leu Asp Ser Asp	Gly Trp Leu His Thr	Gly Asp Ile Gly Arg	Trp		
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn	Ile		
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile	Glu		
	605		610		615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His  
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Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp  
635 640 645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly  
650 655 660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile  
665 670 675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr  
680 685 690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser  
695 700 705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly  
710 715 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu  
725 730 735

His Ile Gln Asp

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

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<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

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<400> 88
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          35          40          45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
          50          55          60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
          65          70          75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
          80          85          90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
          95          100         105
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
          110         115         120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
          125         130         135

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Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu			

	425		430		435
Asp Pro Ala Leu	Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu	Gly		
	440	445	450		
Trp Val Leu Arg	Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro	Lys		
	455	460	465		
Trp Pro Thr Pro	Glu Lys Leu Trp Asp	Trp Asp Met Trp Met	Arg		
	470	475	480		
Met Pro Glu Gln	Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp	Val		
	485	490	495		
Ser Arg Ser Tyr	His Phe Gly Ile Val	Gly Leu Asn Met Asn	Gly		
	500	505	510		
Tyr Phe His Glu	Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr	Val		
	515	520	525		
Pro Gly Val Gln	Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu	Ala		
	530	535	540		
Tyr Glu Val Glu	Val His Arg Leu Leu	Ser Glu Ala Glu Val	Leu		
	545	550	555		
Asp His Ser Lys	Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp	Thr		
	560	565	570		
Glu Gly His Thr	Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp	Asp		
	575	580	585		
Asp Phe Thr Thr	Trp Thr Gln Leu Ala	Lys Cys Leu His Ile	Trp		
	590	595	600		
Asp Leu Asp Val	Arg Gly Asn His Arg	Gly Leu Trp Arg Leu	Phe		
	605	610	615		
Arg Lys Lys Asn	His Phe Leu Val Val	Gly Val Pro Ala Ser	Pro		
	620	625	630		
Tyr Ser Val Lys	Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu	Glu		
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Pro Pro Pro Lys	Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln	Thr		
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<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

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<210> 90  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 90  
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<210> 91  
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<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
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<223> Synthetic construct.

<400> 91  
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<210> 92  
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<212> DNA  
<213> Artificial

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<223> Synthetic construct.

<400> 92  
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<210> 93  
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<213> Artificial

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<221> Artificial sequence  
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<223> Synthetic construct.

<400> 93  
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<210> 94  
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<212> DNA  
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<400> 94

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<211> 307  
<212> PRT  
<213> Homo sapiens

<400> 95  
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Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
35 40 45  
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
50 55 60  
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
65 70 75  
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
80 85 90  
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
95 100 105  
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
110 115 120  
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
125 130 135  
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
140 145 150  
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
155 160 165  
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
170 175 180  
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
185 190 195  
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
200 205 210  
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
215 220 225  
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240									
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
	245								250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
	260								265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
	275								280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
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Leu	Ser	Val	Gly	His	Gln	His								
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<210> 96
<211> 25
<212> DNA
<213> Artificial
<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.
<400> 96
ggtgtgggtg aataaaggag ggcag 25

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<210> 97
<211> 25
<212> DNA
<213> Artificial
<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.
<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Artificial
<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct.

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<210> 99
<211> 1429

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<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150  
ccgcccctcg tgctggccgc cctggtggcc tgcattcatcg tcttgggctt 200  
caactactgg attgagagct cccggagcgt ggacctccag acacggatca 250  
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gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
				20					25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
				35					40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
				50					55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
				65					70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
				80					85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
				95					100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
				110					115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
				125					130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
				140					145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
				155					160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
				170					175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
				185					190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
				200					205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
				215					220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
				230					235					240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101  
 <211> 3671  
 <212> DNA  
 <213> Homo sapiens

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<210> 102  
 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
				170					175					180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
				185					190					195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500	505		510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515	520		525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530	535		540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545	550		555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560	565		570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575	580		585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590	595		600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605	610		615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620	625		630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635	640		645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650	655		660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665	670		675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680	685		690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695	700		705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710	715		720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725	730		735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740	745		750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755	760		765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770	775		780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr



	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala	Ala
	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala	Ala Met Val Thr Ala	Leu
	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu	Leu His Ala Glu Arg	Ile
	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu	Leu
	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro	Phe
	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala	Trp Ala Leu Met Ala	Thr
	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln	Pro Val Phe Pro Ala	Ile
	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe	Pro Glu Gly His Gly	Ser
	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe	Ala
	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu	Trp
	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln	Pro
	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	Glu
	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg	Asp Ala Pro Gln His	Phe
	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile	Leu
	1010	1015	1020
Gly Ile Gln Ile	Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu	Arg
	1025	1030	1035
Arg His Leu Met	Val Trp Lys Val Phe	Ala Pro Lys Phe Ile	Phe
	1040	1045	1050
Glu Ala Val Gly	Phe Ile Val Ser Ser	Val Gly Leu Leu Leu	Gly
	1055	1060	1065
Ile Ala Leu Val	Met Arg Val Asp Gly	Ala Val Ser Ser Trp	Phe
	1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103

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cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350  
taaatacaaac agaacgtggg cccagtgtgt gaccaaccac acgctgggtg 400  
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cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
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 cgtgtgtgat tgggtcatgc atgtaggtct cttacaatg atggtgggcc 1650  
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<210> 104  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
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 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu  
 20 25 30  
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
 35 40 45  
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
 50 55 60  
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
 65 70 75  
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
 80 85 90  
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val  
 95 100 105  
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro  
 110 115 120  
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu  
 125 130 135  
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile  
 140 145 150  
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr  
 155 160 165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile		170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys		185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys		200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val		215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro		230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu		245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser		260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys		275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys		290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser		305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu		320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp		335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro		350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr		365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser		380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly		395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro		410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly		425	430	435
Leu	Tyr	Val	Gln	Met	Glu	Asn										440		

<210> 105

<211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
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 <222> 1-21  
 <223> Synthetic construct  
  
 <400> 105  
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 <210> 106  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 106  
 cagtgtgccca ggactttg 18  
  
 <210> 107  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 107  
 agtcgcaggc agcgttgg 18  
  
 <210> 108  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 108  
 ctctccgag tctgtgtgct cctgc 25  
  
 <210> 109  
 <211> 51  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

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c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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cggcagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttctctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcctcagcc 300

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actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400

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tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
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Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg  
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg  
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly  
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val  
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
 275 280

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 112  
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<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 113  
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<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-44  
 <223> Synthetic construct.

<400> 114  
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<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
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 gctcattt 1808

<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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 20 25 30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
 35 40 45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
 95 100 105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
 110 115 120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
 125 130 135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
 140 145 150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
 155 160 165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
 170 175 180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
 185 190 195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
 200 205 210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 117

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala  
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr  
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg  
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala  
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu  
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe  
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His  
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr  
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly  
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn  
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser  
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr  
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly  
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu  
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser  
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala  
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttcctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

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tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
 gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
 ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400  
 gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
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 ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550  
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
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 cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750  
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 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650



gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
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<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123

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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
				170					175					180
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly

	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr			
	245	250		255	
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp			
	260	265		270	
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly			
	275	280		285	
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtggt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150  
tgagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
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agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
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acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400  
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<210> 128  
<211> 484  
<212> PRT  
<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro	Val	Ser	Gln														

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129

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cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

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<210> 130

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<211> 335

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<212> PRT

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<213> Homo sapiens

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<400> 130

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Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
  1             5             10             15

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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
      20             25             30

```

```

Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
      35             40             45

```

```

Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
      50             55             60

```

```

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
      65             70             75

```

```

Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
      80             85             90

```

```

Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
      95             100            105

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Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 ctgctaggga gagaacgcca gagggaggcg gctggcccg cggcaggctc 100



tcagaaccgc tacggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
 cttggcgctg gcggtactgg ccccgaggc aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250  
 aggttaacat ttcattcagg aagtcaggta gtgaaacttc cttttatcaa 300  
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
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 atggatggat gtcatggaga ggcattggcta ccgaacacag aaatttggga 500  
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 tttattggct tgaaaaagt tctcatgatg ccatcaaaat cccaaagtgg 850  
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 gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150  
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 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250  
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 gtcaaaaacc tgcattccac ctggattctg agtgaattcc atggatgtaa 1350  
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400  
 cctattcgga tgggtgcatc atattgcctc aactctttga tctttcctcg 1450  
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500  
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

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cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagt 1750
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atgaaacagt tttataaatt accaagtttt ggccgggcac agtggctcac 1850
acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
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agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
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aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250
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atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

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<400> 132
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Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
          20          25          30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
          35          40          45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
          50          55          60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
          65          70          75

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Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

	365		370		375
Leu Ser Gly Tyr	Ser 380	Leu Leu Pro Leu	Ser 385	Ser Glu Thr Phe	Lys 390
Asn Glu His Lys	Val 395	Lys Asn Leu His	Pro 400	Pro Trp Ile Leu	Ser 405
Glu Phe His Gly	Cys 410	Asn Val Asn Ala	Ser 415	Thr Tyr Met Leu	Arg 420
Thr Asn His Trp	Lys 425	Tyr Ile Ala Tyr	Ser 430	Asp Gly Ala Ser	Ile 435
Leu Pro Gln Leu	Phe 440	Asp Leu Ser Ser	Asp 445	Pro Asp Glu Leu	Thr 450
Asn Val Ala Val	Lys 455	Phe Pro Glu Ile	Thr 460	Tyr Ser Leu Asp	Gln 465
Lys Leu His Ser	Ile 470	Ile Asn Tyr Pro	Lys 475	Val Ser Ala Ser	Val 480
His Gln Tyr Asn	Lys 485	Glu Gln Phe Ile	Lys 490	Trp Lys Gln Ser	Ile 495
Gly Gln Asn Tyr	Ser 500	Asn Val Ile Ala	Asn 505	Leu Arg Trp His	Gln 510
Asp Trp Gln Lys	Glu 515	Pro Arg Lys Tyr	Glu 520	Asn Ala Ile Asp	Gln 525
Trp Leu Lys Thr	His 530	Met Asn Pro Arg	Ala 535	Val	

<210> 133  
 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
 catcaccagc tgtgacatct atagcacctt tctgggcctg cccgctgaca 350  
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctcctccctg 400  
 gcctgcatta tctctgtggg gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500  
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cagggtatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850  
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cccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200  
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actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400  
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gcagcctggg acatttaaaa aaata 1475

<210> 134  
<211> 230  
<212> PRT  
<213> Homo sapiens

<400> 134  
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Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp  
20 25 30  
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
35 40 45  
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

	50		55		60
Ile Thr Gln Cys Asp	65	Ile Tyr Ser Thr	70	Leu Leu Gly Leu Pro	75
Asp Ile Gln Ala Ala	80	Gln Ala Met Met	85	Val Thr Ser Ser Ala	90
Ser Ser Leu Ala Cys	95	Ile Ile Ser Val	100	Val Gly Met Arg Cys	105
Val Phe Cys Gln Glu	110	Ser Arg Ala Lys	115	Asp Arg Val Ala Val	120
Gly Gly Val Phe Phe	125	Ile Leu Gly Gly	130	Leu Leu Gly Phe Ile	135
Val Ala Trp Asn Leu	140	His Gly Ile Leu	145	Arg Asp Phe Tyr Ser	150
Leu Val Pro Asp Ser	155	Met Lys Phe Glu	160	Ile Gly Glu Ala Leu	165
Leu Gly Ile Ile Ser	170	Ser Ser Leu Phe	175	Ser Leu Ile Ala Gly	180
Leu Cys Phe Ser Cys	185	Ser Ser Gln Arg	190	Asn Arg Ser Asn Tyr	195
Asp Ala Tyr Gln Ala	200	Gln Pro Leu Ala	205	Thr Arg Ser Ser Pro	210
Pro Gly Gln Pro Pro	215	Lys Val Lys Ser	220	Glu Phe Asn Ser Tyr	225
Leu Thr Gly Tyr Val	230				

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 aagtcacgcg tcccgtggc tcagaacat ggctgtgcca gccggcaccc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcca atgtgggtccc cctgcacct 250  
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 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
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 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
 65 70 75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
 80 85 90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
 95 100 105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
 110 115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

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 agaactgcga ctcagcccg acctcggatg acaggctttg tcgcagtgtc 350  
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 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

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			20					25						30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105
Cys	Arg	Ser	Val	Ser										
			110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139



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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggctgc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttcctg gctgcgtccc taggtccggt ggcagccttc aaggctcgca 250  
 cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300  
 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350  
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 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
 gtccgcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
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 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700  
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 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 ataaccgagg ccaaagtcag gcaccccctg tcctatgtgg cccagcgcca 950  
 gccttctgag tctgggcggc atctgcttcc ggagcccagc acccccctgt 1000  
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggtt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctgggtccc tcctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500  
 ccccggtggcc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550  
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgcca 1600  
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650  
 gatctgtcaa cagggttaagt caatctgggg cttccactgc ctgcattcca 1700  
 gtccccagag cttggtgggc ccgaaacggg aagtacatat tggggcatgg 1750  
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850  
 ggggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900  
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly  
 1 5 10 15  
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val  
 20 25 30  
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

	140		145		150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu	155		160		165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val	170		175		180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala	185		190		195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu	200		205		210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg	215		220		225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile	230		235		240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro	245		250		255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln	260		265		270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 cccacgcgctc cgcgcctctc cttctgctg gaccttcctt cgtctctcca 50  
 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100  
 cttagacctc cttcctgcc ctcctttcct gccaccgct gcttcctggc 150  
 cttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250  
 ccgctcccgg accagcggcc tgaccctggg gaaaggatgg ttcccagagt 300  
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450



Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450
Thr		

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
 ctagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50  
 cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100  
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccc 400  
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccgggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
 35 40 45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
 50 55 60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
 65 70 75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
 80 85 90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50  
 ttgaggggaa gaggtgact gtacgttcct tctactctgg caccactctc 100  
 caggctgcc a tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
tggaggccct gggaccaaag gcaaggaag aaggaatgag aagtacgata 500  
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600  
gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650  
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700  
gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggg 750  
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
aaccgaacag tgggtggacag ctcaagtatt ccagcagagg ggctgatccc 900  
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
tctatgtcgt ctataacacc cgtcctgcca gtccggcccg catccagtgc 1150  
tcctttgatg ccagcggcac cctgacccct gaacgggcag cactccctta 1200  
ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
catctttctc actcccatac atttatatta tatccccact aaatttcttg 1400  
ttcctcattc ttcaaagtgt ggccagttgt ggctcaaata ctctatatatt 1450  
ttagccaatg gcaatcaaat tctttcagct ctttgtttc atacggaact 1500  
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600  
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650  
agcagtgttc ttccctcag agtgacttgg ggaggagaa ataggaggag 1700  
acgtccagct ctgtcctctc ttccctactc ctcccttcag tgtcctgagg 1750  
aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850



aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp  
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met  
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn  
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala  
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu  
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro  
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys  
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys  
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg  
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln  
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala  
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala  
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr  
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro  
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser  
245 250 255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50  
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100  
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt ottactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actggggtca gttcctctca 600  
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggg tccccgggc cacagcgaag tggaaaggtc cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggccgtgttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850  
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950  
 ttctttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100  
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa 1400  
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500  
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550  
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
 acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg 1750  
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800  
 atgggagtca ggtgtcatgg ctgccctgag ctgggagggga agaaggctga 1850  
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly  
1 5 10 15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala  
20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

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<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcgggc gcggttgccg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcgggcg ggaatgtcac cggtagggcg ggggccgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggccc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

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caccctcttt tgggogactg ctggaccctc ttccaccacc tttcaggcgc 450  
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500  
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550  
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600  
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650  
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700  
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750  
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800  
gaaacctgca aagagggcct ttacctaaat tacacttctg ggctctgtca 850  
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaacaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaacaa aggaggatga 1000  
gggtcataga ttacaaaat attttatata cttttattct cttactttat 1050  
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100  
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150  
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggct 1200  
ttcaggcatg aaacctgcta ggaggttttag aaatgttctt atgtttatta 1250  
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300  
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350  
ggtaccctaa tttatttaac tagtggttag tagactgggt ttactctatt 1400  
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
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tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550  
tatgtgaggc acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600  
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tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700  
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750  
taaataagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
ctgggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900  
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
 ctcacgcctg taatcctagc actttgggag gcccaaggcgg gtggatcact 2050  
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctct 2100  
 ctactaaaaa tacaacaaaa ttagctgggc gtggtggcac acacctgtag 2150  
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250  
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				



	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255
Cys Asn Arg					

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
 <400> 154  
 aactgctctg tggttggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
 <400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 agggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgacag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggctttt ggtctcgggtg cccagggccc aggccgtgtg gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
 ccgggaaaag ggcttttgcca tggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcca tcatcttcac tcagctggag 400  
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600  
 gggtcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
     1                    5                    10                    15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
                     20                    25                    30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
                     35                    40                    45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
                     50                    55                    60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
                     65                    70                    75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
                     80                    85                    90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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aacagacggt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggccctgtgt 150
gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacct 200
tggcccagta gttcatggct actgggttccg ggaagggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tactttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtgact caggggggtgg tcggggggagc 1100
tggagccaca gccctgggtct tcctgtcctt ctgcgtcatc ttcgttgtag 1150
tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatag aggatgcaaa cgctgtcagg gggttcagcct ctcagggggcc 1250
cctgactgaa ccttggggcag aagacagtcc cccagaccag cctccccag 1300
cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
agcttccaga tggatgaagcc ttgggactcg cggggacagg aggccactga 1400
caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
acagacaaat tccta 1665

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<210> 160
<211> 463
<212> PRT
<213> Homo sapiens

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<400> 160
Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
  1          5          10          15
Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
          20          25          30
Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
          35          40          45
Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
          50          55          60
Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
          65          70          75
Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
          80          85          90
Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
          95          100         105
Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

```

	110		115		120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	125		130		135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140		145		150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155		160		165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170		175		180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185		190		195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200		205		210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215		220		225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230		235		240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245		250		255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260		265		270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275		280		285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290		295		300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305		310		315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320		325		330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335		340		345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350		355		360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365		370		375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380		385		390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395		400		405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgcc tgtccttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200  
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250  
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcccc ggaggggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550  
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcctt 650  
 gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

	20	25	30
Val Lys Ala Met	Val Val Asp Lys Asp	Phe Pro Glu Asp Arg Arg	
35	40	45	
Pro Arg Lys Val	Ser Pro Val Lys Val	Thr Ala Leu Gly Gly Gly	
50	55	60	
Lys Leu Glu Ala	Thr Phe Thr Phe Met	Arg Glu Asp Arg Cys Ile	
65	70	75	
Gln Lys Lys Ile	Leu Met Arg Lys Thr	Glu Glu Pro Gly Lys Tyr	
80	85	90	
Ser Ala Tyr Gly	Gly Arg Lys Leu Met	Tyr Leu Gln Glu Leu Pro	
95	100	105	
Arg Arg Asp His	Tyr Ile Phe Tyr Cys	Lys Asp Gln His His Gly	
110	115	120	
Gly Leu Leu His	Met Gly Lys Leu Val	Gly Arg Asn Ser Asp Thr	
125	130	135	
Asn Arg Glu Ala	Leu Glu Glu Phe Lys	Lys Leu Val Gln Arg Lys	
140	145	150	
Gly Leu Ser Glu	Glu Asp Ile Phe Thr	Pro Leu Gln Thr Gly Ser	
155	160	165	
Cys Val Pro Glu	His		
170			

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-21  
 <223> Synthetic construct.  
  
 <400> 165  
 gtcctccgga aagtccttat c 21  
  
 <210> 166  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 166  
 gcctagtgtt cgggaacgca gcttc 25  
  
 <210> 167  
 <211> 50  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.  
  
 <400> 167  
 caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50  
  
 <210> 168  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 168  
 ctgtccttca ccctggagga ggaggatata acaggacct ggtac 45  
  
 <210> 169  
 <211> 1204  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 169



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cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccgacag ccactgagtc cttccccac cccggcttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500
ctcacgtgtg gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag ccccgagtta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcacctc catttccact 900
tggtgtttgg ttcctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
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aaaa 1204

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<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

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<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
  1             5             10             15

```

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro		20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu		35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala		50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His		65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr		80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys		95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val		110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys		125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr		140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn		155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly		170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly		185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn		200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala		215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val		230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn							245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc ggggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
 <400> 176  
 cccttgatga tcctgggtc 18  
 <210> 177  
 <211> 50  
 <212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.  
 <400> 177  
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50  
 <210> 178  
 <211> 43  
 <212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.  
 <400> 178  
 gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43  
 <210> 179  
 <211> 907  
 <212> DNA  
 <213> Homo sapiens  
 <400> 179  
 gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50  
 gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100  
 aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150  
 agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200  
 atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250  
 caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcac 300  
 aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350  
 aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
 tgtgaccaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650  
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
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 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens  
 <400> 180  
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 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu  
 20 25 30  
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn  
 35 40 45  
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr  
 50 55 60  
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg  
 65 70 75  
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly  
 80 85 90  
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro  
 95 100 105  
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly  
 110 115 120  
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu  
 125 130 135  
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser  
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 181  
 gtgttctgct ggagccgatg cc 22

<210> 182  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 182  
 gacatggaca atgacagg 18

<210> 183  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 183  
 cctttcagga tgtaggag 18

<210> 184  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 184  
 gatgtctgcc accccaag 18  
  
 <210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.  
  
 <400> 185  
 gcatcctgat atgacttgat acgtggc 27  
  
 <210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 186  
 tacaagaggg aagaggagtt gcac 24  
  
 <210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-52  
 <223> Synthetic construct.  
  
 <400> 187  
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
  
 cc 52  
  
 <210> 188  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 188  
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50  
  
 ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

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cccaaagtct tctgtgtca ataactca ctgcacctgc aacctggat 150
atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
aacgccaggc atgggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaaatcg 400
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
ccaaataaag taottatatt ctc 573

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<210> 189
<211> 74
<212> PRT
<213> Homo sapiens
<400> 189
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  1          5          10          15
Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
          20          25          30
Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
          35          40          45
Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
          50          55          60
Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
          65          70

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<210> 190
<211> 24
<212> DNA
<213> Artificial
<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

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<400> 190
agggaccatt gcttcttcca ggcc 24

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<210> 191
<211> 24
<212> DNA
<213> Artificial

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<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcagggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
ggtgggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
gactttggaa gtgaaccacc atgggggtca gcatcttttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500  
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600  
tgccctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700  
atgcctgcca gggtgattct gggggcccc tggtgtgtgg gggagtccct 750  
caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
 gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser
1				5					10					15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg
				20					25					30
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu
				35					40					45
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala
				50					55					60
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His
				65					70					75
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly
				80					85					90
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His
				95					100					105
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val
				110					115					120
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr
				125					130					135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His
				140					145					150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser
				155					160					165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile
				170					175					180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala
				185					190					195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
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 ctcgctccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100  
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150  
 ggcttgcctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
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 caagaccac ctggagatga agaagatgat ctgagaggtg acaggagggg 400  
 tcagtgcac tatatcctac cgagactttg tgaacatgat gctggggaaa 450  
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
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 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350  
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450  
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

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Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu	35	40	45	
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp	50	55	60	
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met	65	70	75	
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys	80	85	90	
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr	95	100	105	
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu	110	115	120	
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro	125	130	135	
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro	140	145	150	

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
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caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350  
tgcattctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400  
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ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500  
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acaacaacat cagtcgcata ctggtcacca gcttcaacca catgccgaag 700  
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	



Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	
				170					175					180	
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg	
				185					190					195	
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	
				200					205					210	
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	
				215					220					225	
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	
				230					235					240	
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	
				245					250					255	
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	
				260					265					270	
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	
				275					280					285	
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	
				290					295					300	
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	
				305					310					315	
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	
				320					325					330	
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	
				335					340					345	
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	
				350					355					360	
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	
				365					370					375	
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	
				380					385					390	
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	
				395					400					405	
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	
				410					415					420	
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	
				425					430					435	
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	
				440					445					450	
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser	

	455		460		465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470	475			480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe				
	485	490			495
Ser Ser Glu Cys	Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg				
	500	505			510
Cys Glu Gly Thr	Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg				
	515	520			525
Ile Pro Ser His	Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn				
	530	535			540
Asp Asn Glu Val	Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys				
	545	550			555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys				
	560	565			570
Glu Val Arg Glu	Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu				
	575	580			585
Leu Met Leu Thr	Gly Asn Gln Leu Glu Thr Val His Gly Arg Val				
	590	595			600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn				
	605	610			615
Leu Ile Ser Cys	Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser				
	620	625			630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr				
	635	640			645
Pro Gly Ala Phe	Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu				
	650	655			660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly				
	665	670			675
Lys Trp Leu Arg	Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys				
	680	685			690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala				
	695	700			705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln				
	710	715			720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val				
	725	730			735
Val Arg Cys Ser	Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met				
	740	745			750



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Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser  
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
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caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
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gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
                   20                  25                  30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
                   35                  40                  45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
                   50                  55                  60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
                   65                  70                  75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
                   80                  85                  90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
                   95                  100                  105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
                   110                  115                  120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
                   125                  130                  135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
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<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
ctcattggct gcctggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
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<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
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cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100  
tattaataact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250



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acattatcag	gaattgaaga	aaatgggtcca	acagtccgac	cttggccagt	700
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$\langle 210 \rangle$  210

<211> 323

<212> PRT  
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211  
 <211> 1554  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
 cttcgcgatc ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc 100  
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
 tttgcatgag ttcttggtta atttgcatga gagatatggg cctgtggtct 250  
 ccttctggtt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300  
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400  
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tgggtacttca ggatcctaatt acttggccat ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550

ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1				5					10					15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu

Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser
				155					160					165
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val
				170					175					180
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln
				185					190					195
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu
				200					205					210
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu
				215					220					225
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys
				230					235					240
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser
				245					250					255
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser
				260					265					270
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys
				275					280					285
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys
				290					295					300
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val
				305					310					315
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu
				320					325					330
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln
				335					340					345
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg
				350					355					360
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro
				365					370					375
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp
				380					385					390
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly
				395					400					405
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr
				410					415					420
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val
				425					430					435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
455 460

<210> 213  
<211> 759  
<212> DNA  
<213> Homo sapiens

<400> 213  
ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50  
tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100  
tcagggttg tgccctctcg cttcctgacg ctctggcgc atctggtggt 150  
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
gccgcgctct ctgtcacct gggcctcttt gcagtggagc tggccgggtt 300  
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400  
tgaggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450  
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600  
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
tgttttgtag taacattaag acttatatac agtttttagg gacaattaa 750  
aaaaaaaa 759

<210> 214  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 214  
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
1 5 10 15  
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	50	55	60
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	65	70	75
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	80	85	90
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	95	100	105
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	110	115	120
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	125	130	135
Lys	Lys	Lys	Pro	Phe											140		

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccggaccc tgccgccctg ccactatgtc ccgccgtct atgctgcttg 50  
 cctgggctct cccagcctc cttcgactcg gagcggtca ggagacagaa 100  
 gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
 ggcatcagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450  
 ccaggccatc cgggcagccc agggcttact ggcctgcggt gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccgga tgtgcagcgt 550  
 aactctctc caggcaacca gctctaccac ctcattcaga attggccaca 600  
 ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu  
1 5 10 15  
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys  
20 25 30  
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu  
35 40 45  
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser  
50 55 60  
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln  
65 70 75  
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp  
80 85 90  
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val  
95 100 105  
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His  
110 115 120  
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr  
125 130 135  
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly  
140 145 150  
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr  
155 160 165  
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly  
170 175 180  
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser  
185 190 195  
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50  
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100  
tctatctggt catctgtggc caggatgatg gtcctcccgg ctcagaggac 150  
cctgagcgtg atgaccacga gggccagccc cggccccggg tgccctcgaa 200



gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250  
 tagggctgct ggccccgcct ggggaggett ggggcattct tgggcagccc 300  
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350  
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400  
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450  
 cacttccaac acaatgccac agggcaggga aacatctcca tcagcctcgt 500  
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550  
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600  
 gaacgggggc gccggacctc gctttgcacc cacgaccag ccaagatctg 650  
 ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700  
 tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggtg 750  
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800  
 cccatctggg tgaccggggg caggccacag agggcaggcc agggctggaa 850  
 ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900  
 gttgggcctc aggcaggag ggggggtggag acgaggagat gccaagtggg 950  
 gccagggcca agtctcaagt ggcagagaaa ggggtccaag tgctgggtccc 1000  
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100  
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
 gtcattggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200  
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250  
 atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtggg 1300  
 gccagaggag ctctccagcc ctgcctagt ggcgccctga gcccttgtc 1350  
 gtgtgctgag catggcatga ggctgaagt gcaaccctgg ggtctttgat 1400  
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450  
 ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500  
 cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550  
 acagcccatc cgcgtgctgt gtgtccctct tccaccccaa ccctgctgg 1600  
 ctctctggg agcatccatg tcccgagag gggtcctca acagtcagcc 1650

tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cgccctctca 1700  
gcagcgggca cgggtggggc ggggcggggc cgcagagcat gtgctggatc 1750  
tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800  
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
aataaagctt gccccggggc a 1871

<210> 218  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 218  
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser  
1 5 10 15  
Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser  
20 25 30  
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg  
35 40 45  
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
50 55 60  
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
65 70 75  
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
80 85 90  
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
95 100 105  
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
110 115 120  
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
125 130 135  
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
140 145 150  
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
155 160 165  
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
170 175 180  
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
185 190 195  
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50  
 gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100  
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200  
 gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250  
 tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300  
 agcgccagcc ggctgcggtt gccacacgg ctcaccatgg gctccggggc 350  
 ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400  
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
 aagtgtctgg tgggtgtgca ctcgaaccgg gccacggact ccaagggctc 500  
 ctcttcctcc ccgctgggga tatcggtccg ggccggccaac tccaaggtcg 550  
 ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650  
 tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
 tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750  
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
 tgttactcgt gaagctgcca cgaatgggtg cctgctctac ctagataaag 850  
 aggataagggt ttacctaaaa ctggagaaaag gtaatttggg tggaggctgg 900  
 cagtattcca cgttttctgg ctttctgggtg ttccccctat aggattcaat 950  
 ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000  
 gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
 ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
 aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200  
 acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
 gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300  
 gaaaactcta aagttctgac ttcaatcaac ggtagtggtg atactgccaa 1350  
 agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
 ggaattagtt tgtttgggtc ttgtaaaaaa cttggatttt ttttttcagt 1450  
 aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500  
 aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaaa 1550  
 gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataatttt 1600  
 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650  
 aaagttgctt acccaaaatc taagtgtca atccctgagc ctcagcaaaa 1700  
 cagctcccct ccgagggaaa tottatactt tattgctcaa ctttaattaa 1750  
 aatgattgat aataaccact ttattaaaaa cctaaggttt tttttttttc 1800  
 cgtagacatg accactttat taactgggtg tgggatgctg ttgtttctaa 1850  
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctggttt 1900  
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950  
 ttcaaataat ccataatctaa atttagtgca atatcttgct ttttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

<210> 220  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 220  
 Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu  
 1 5 10 15  
 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp  
 20 25 30  
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
 35 40 45  
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
 50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
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<210> 221

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 221

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<210> 222

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 222

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<210> 223

<211> 40

<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

<400> 223  
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<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
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tatcatcttc ctcatgccg gagctttctt ctggttggtg tctctactga 150  
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
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gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350  
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tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600  
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650  
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700  
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actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850  
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900  
ta 902

<210> 225  
<211> 257  
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly  
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Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu  
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Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser  
35 40 45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile  
50 55 60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly  
65 70 75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr  
80 85 90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn  
95 100 105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser  
110 115 120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn  
125 130 135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly  
140 145 150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val  
155 160 165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly  
170 175 180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr  
185 190 195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly  
200 205 210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr  
215 220 225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu  
230 235 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg  
245 250 255

Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200  
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

320					325					330				
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				335					340					345
Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly
				350					355					360
Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser
				365					370					375
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg	Ser	Phe
				380					385					390
Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val
				395					400					405
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys
				410					415					420
Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala
				425					430					435
Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe
				440					445					450
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val
				455					460					465
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn
				470					475					480
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly
				485					490					495
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile
				500					505					510
Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile
				515					520					525
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu
				530					535					540
Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr
				545					550					555
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys
				560					565					570
Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met
				575					580					585
Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro
				590					595					600
Asp	Ile	Asn	Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile
				605					610					615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	620	625	630
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	635	640	645
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	650	655	660
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	665	670	675
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	680	685	690
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	695	700	705
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	710	715	720
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	725	730	735
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	740	745	750
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	755	760	765
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	770	775	780
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	785	790	795
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	800	805	810
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	815	820	825
Arg	Asp	Lys	Ile	Tyr	Val	Phe									830		

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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 gtgggcacgg tccctacagc ttcacccttg gtcccaacct cacggtgcaa 2200  
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 gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc 2350  
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 tcccctggga gagagcccag caccgaagat ccagcagggg acaggacaga 2650  
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 ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750  
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1				5					10					15

Ala	Leu	Pro	Lys	Ala	Gln	Pro	Ala	Glu	Leu	Ser	Val	Glu	Val	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	20		25		30
Glu Asn Tyr Gly	Gly Asn Phe Pro Leu Tyr	Leu Thr Lys Leu Pro			
	35	40		45	
Leu Pro Arg Glu	Gly Ala Glu Gly Gln Ile	Val Leu Ser Gly Asp			
	50	55		60	
Ser Gly Lys Ala	Thr Glu Gly Pro Phe Ala	Met Asp Pro Asp Ser			
	65	70		75	
Gly Phe Leu Leu	Val Thr Arg Ala Leu Asp	Arg Glu Glu Gln Ala			
	80	85		90	
Glu Tyr Gln Leu	Gln Val Thr Leu Glu Met	Gln Asp Gly His Val			
	95	100		105	
Leu Trp Gly Pro	Gln Pro Val Leu Val His	Val Lys Asp Glu Asn			
	110	115		120	
Asp Gln Val Pro	His Phe Ser Gln Ala Ile	Tyr Arg Ala Arg Leu			
	125	130		135	
Ser Arg Gly Thr	Arg Pro Gly Ile Pro Phe	Leu Phe Leu Glu Ala			
	140	145		150	
Ser Asp Arg Asp	Glu Pro Gly Thr Ala Asn	Ser Asp Leu Arg Phe			
	155	160		165	
His Ile Leu Ser	Gln Ala Pro Ala Gln Pro	Ser Pro Asp Met Phe			
	170	175		180	
Gln Leu Glu Pro	Arg Leu Gly Ala Leu Ala	Leu Ser Pro Lys Gly			
	185	190		195	
Ser Thr Ser Leu	Asp His Ala Leu Glu Arg	Thr Tyr Gln Leu Leu			
	200	205		210	
Val Gln Val Lys	Asp Met Gly Asp Gln Ala	Ser Gly His Gln Ala			
	215	220		225	
Thr Ala Thr Val	Glu Val Ser Ile Ile Glu	Ser Thr Trp Val Ser			
	230	235		240	
Leu Glu Pro Ile	His Leu Ala Glu Asn Leu	Lys Val Leu Tyr Pro			
	245	250		255	
His His Met Ala	Gln Val His Trp Ser Gly	Gly Asp Val His Tyr			
	260	265		270	
His Leu Glu Ser	His Pro Pro Gly Pro Phe	Glu Val Asn Ala Glu			
	275	280		285	
Gly Asn Leu Tyr	Val Thr Arg Glu Leu Asp	Arg Glu Ala Gln Ala			
	290	295		300	
Glu Tyr Leu Leu	Gln Val Arg Ala Gln Asn	Ser His Gly Glu Asp			
	305	310		315	



Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	320	325	330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	335	340	345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	350	355	360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	365	370	375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	380	385	390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	395	400	405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	410	415	420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	425	430	435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	440	445	450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	455	460	465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	470	475	480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	485	490	495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	500	505	510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	515	520	525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	530	535	540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	545	550	555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	560	565	570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	575	580	585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	590	595	600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly			

	605	610	615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp
	620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu
	635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His
	650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser
	665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val
	680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr
	695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile
	710	715	720
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val
	725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg
	740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val
	755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile
	770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp
	785	790	795
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val	
	800	805	

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 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 230  
 cgccttaccg cgcagcccgga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Artificial Sequence  
 <222> full  
 <223> Synthetic oligonucleotide probe

<400> 231  
 cctgagctgt aaccccactc cagg 24

<210> 232  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 232  
 agagtctgtc ccagctatct tgt 23

<210> 233  
 <211> 2786  
 <212> DNA  
 <213> Homo sapiens

<400> 233  
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 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
 gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250  
 atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300  
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
 agtaataact tcaactacgg ggcttaccat tccctggaag ctattttacca 400  
 cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450  
 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
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 ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
1				5					10					15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly Lys Gly Val	Arg Arg Pro Ala Val	Trp Leu Asn Ala Gly	Ile
170		175	180
His Ser Arg Glu	Trp Ile Ser Gln Ala	Thr Ala Ile Trp Thr	Ala
185		190	195
Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr	Ser
200		205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn	Pro
215		220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg	Lys
230		235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp	Pro
245		250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser	Asp
260		265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser	Glu
275		280	285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly	Asn
290		295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu	Met
305		310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu	Glu
320		325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser	Val
335		340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val	Tyr
350		355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly	Ile
365		370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr	Gly
380		385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu	Thr
395		400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn	Leu
410		415	420

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200  
aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250  
gagtcagaac atcttcttct ccctgtgag tgtctccact tccctggcca 300  
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350  
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ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450  
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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
1				5					10					15
Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20					25					30
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35					40					45
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50					55					60
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65					70					75
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80					85					90
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95					100					105
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110					115					120
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125					130					135
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140					145					150
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155					160					165
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170					175					180
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185					190					195
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala



200					205					210				
Lys	Trp	Glu	Lys	Pro	Phe	His	Leu	Glu	Tyr	Thr	Arg	Lys	Asn	Phe
				215					220					225
Pro	Phe	Leu	Val	Gly	Glu	Gln	Val	Thr	Val	Gln	Val	Pro	Met	Met
				230					235					240
His	Gln	Lys	Glu	Gln	Phe	Ala	Phe	Gly	Val	Asp	Thr	Glu	Leu	Asn
				245					250					255
Cys	Phe	Val	Leu	Gln	Met	Asp	Tyr	Lys	Gly	Asp	Ala	Val	Ala	Phe
				260					265					270
Phe	Val	Leu	Pro	Ser	Lys	Gly	Lys	Met	Arg	Gln	Leu	Glu	Gln	Ala
				275					280					285
Leu	Ser	Ala	Arg	Thr	Leu	Ile	Lys	Trp	Ser	His	Ser	Leu	Gln	Lys
				290					295					300
Arg	Trp	Ile	Glu	Val	Phe	Ile	Pro	Arg	Phe	Ser	Ile	Ser	Ala	Ser
				305					310					315
Tyr	Asn	Leu	Glu	Thr	Ile	Leu	Pro	Lys	Met	Gly	Ile	Gln	Asn	Ala
				320					325					330
Phe	Asp	Lys	Asn	Ala	Asp	Phe	Ser	Gly	Ile	Ala	Lys	Arg	Asp	Ser
				335					340					345
Leu	Gln	Val	Ser	Lys	Ala	Thr	His	Lys	Ala	Val	Leu	Asp	Val	Ser
				350					355					360
Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Lys	Phe	Ile
				365					370					375
Val	Arg	Ser	Lys	Asp	Gly	Pro	Ser	Tyr	Phe	Thr	Val	Ser	Phe	Asn
				380					385					390
Arg	Thr	Phe	Leu	Met	Met	Ile	Thr	Asn	Lys	Ala	Thr	Asp	Gly	Ile
				395					400					405
Leu	Phe	Leu	Gly	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ser			
				410					415					

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 238  
ctttgctgtt ggctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 239  
tgactcgggg tctccaaaac cagc 24

<210> 240  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 240  
ggatataggcg gaaggcaaag tcgg 24

<210> 241  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-48  
<223> Synthetic construct.

<400> 241  
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242  
<211> 2436  
<212> DNA  
<213> Homo sapiens

<400> 242  
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 gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

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tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
              20              25              30

Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
              35              40              45

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
              50              55              60

Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
              65              70              75

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Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	80	85	90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	95	100	105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala			

	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic sequence.

<400> 245  
 gtcagagttg gtggctgtgc tagc 24

<210> 246  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 246  
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
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 tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	



Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 251  
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<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

<400> 252

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

80					85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro
				380					385					390
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg
				395					400					405
Glu	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Pro	Asp	Arg	Val	Leu
				410					415					420
Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser
				425					430					435
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala
				440					445					450
Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	Phe
				455					460					465
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly
				470					475					480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly
				485					490					495
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu
				500					505					510
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn
				515					520					525
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp
				530					535					540
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu
				545					550					555
Tyr	Gln	Pro	Gln	Leu	Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu
				560					565					570
Gly	Ala	Ser	Ala	Lys	Asp	Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser
				575					580					585
Pro	Ser	Phe	Val	Pro	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln
				590					595					600
Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser
				605					610					615
Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	Asn	Gly	Ala	Pro	Val	Asn
				620					625					630
Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	Gly	Asp	Leu	Leu	Leu
				635					640					645
Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu
				650					655					660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val

665					670					675				
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	Val	Pro
				680					685					690
Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys
				695					700					705
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
				710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe
				725					730					735
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln
				740					745					750
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu
				755					760					765
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr
				770					775					780
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro
				785					790					795
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile
				800					805					810
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg
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<210> 254

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 254

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<210> 255

<211> 24

<212> DNA

<213> Artificial

<220>

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<222> 1-24

<223> Synthetic construct.

<400> 255  
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<222> 1-18  
<223> Synthetic construct.

<400> 256  
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<211> 41  
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<222> 1-41  
<223> Synthetic construct.

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<210> 258  
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<213> Artificial

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<222> 1-45  
<223> Synthetic construct.

<400> 258  
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<210> 259  
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<400> 259  
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agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150



tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200  
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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			20						25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530										535				540			
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu			
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Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu			
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Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu			
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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln			
				590					595					600			
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu			
				605					610					615			
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys			
				620					625					630			
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg			
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe			
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser			
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Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn			
				680					685					690			
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg			
				695					700					705			
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp			
				710					715					720			
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe			
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Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe			
				740					745					750			
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly			
				755					760					765			
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met			
				770					775					780			
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn			
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<210> 261

<211> 24

<212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
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 <400> 261  
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 <213> Artificial  
  
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 <213> Artificial  
  
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 <213> Homo sapiens  
  
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 tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
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 agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
 agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
 tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500  
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 aataaaaatat tttctattgt agttcaaagt tgccaacatc tttatgtgtc 1350  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys		
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu		
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly		
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val		
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala		
335	340	345

Leu Leu Lys Val Tyr  
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250  
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caggaatcag ttccatgctg tgggtccacct ctacagagat ggggaagact 350  
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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

	20	25	30
Leu Val Gly Glu Asp	Ala Val Phe Ser	Cys Ser Leu Phe Pro	Glu
	35	40	45
Thr Ser Ala Glu Ala	Met Glu Val Arg	Phe Phe Arg Asn Gln	Phe
	50	55	60
His Ala Val Val His	Leu Tyr Arg Asp	Gly Glu Asp Trp Glu	Ser
	65	70	75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg	Thr Glu Phe Val Lys	Asp
	80	85	90
Ser Ile Ala Gly Gly	Arg Val Ser Leu	Arg Leu Lys Asn Ile	Thr
	95	100	105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys	Trp Phe Ser Ser Gln	Ile
	110	115	120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu	Arg Val Ala Ala Leu	Gly
	125	130	135
Ser Leu Pro Leu Ile	Ser Ile Val Gly	Tyr Val Asp Gly Gly	Ile
	140	145	150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp	Phe Pro Gln Pro Thr	Ala
	155	160	165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp	Leu Ser Ser Asp Ser	Arg
	170	175	180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr	Asp Val Glu Ile Ser	Ile
	185	190	195
Ile Val Gln Glu Asn	Ala Gly Ser Ile	Leu Cys Ser Ile His	Leu
	200	205	210
Ala Glu Gln Ser His	Glu Val Glu Ser	Lys Val Leu Ile Gly	Glu
	215	220	225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg	Leu Ala Ser Ile Leu	Leu
	230	235	240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly	Val Val Met Gly Met	Ile
	245	250	255
Ile Val Phe Phe Lys	Ser Lys Gly Lys	Ile Gln Ala Glu Leu	Asp
	260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
	275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys
	290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val	Thr His Arg Lys Ala	Pro
	305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
				395					400					405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
				410					415					420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
				425					430					435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
				440					445					450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
				455					460					465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

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 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
 attttataaa tctccattaa gggaagaatt tgtcaagtct cagggttatca 350  
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450  
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctactcagtt taaaattaaa aaaatcaaca agacagaaac agacagctat 550  
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600  
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 aataccaatc acttcatcat ttaggaagta tgggaactaa gtttaaggaag 1900  
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

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<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269  
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
 35 40 45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
 140 145 150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
 155 160 165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250



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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
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Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
                      20                      25                      30

Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
                      35                      40                      45

Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
                      50                      55                      60

Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
                      65                      70                      75

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Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
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 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250  
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
			20						25					30

Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45

Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60

Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75

Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90

Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105

Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135

Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150

Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165

Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

170					175					180				
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln
				185					190					195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met
				200					205					210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe
				215					220					225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu
				230					235					240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro
				245					250					255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His
				260					265					270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg
				275					280					285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe
				290					295					300
Glu	Met	Glu	Glu	Leu										
				305										

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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cttggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200

agagccagca tggtacagga tcctgacagt gatcaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300

agggtgggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350

attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400

cgggcagcct ctccacttca tcccaggagaa gcagctgtgt gacggagagc 450

tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg  
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser  
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu  
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu  
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu  
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu  
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser  
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys  
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His  
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala  
245 250 255

265

Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
260	265	270	
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
275	280	285	
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
290	295	300	
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
305	310	315	
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
320	325	330	
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
335	340	345	
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
350	355	360	
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
365	370	375	
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
380	385	390	
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
395	400	405	
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
410	415	420	
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	
425	430		

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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gccattctgg ccttgatata ccaggatcca ggggtcccca ggctaaagaa 400



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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

	290		295		300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser	Pro		
	305		310		315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln	Val		
	320		325		330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu	Asp		
	335		340		345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu		
	350		355		360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg		
	365		370		375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr		
	380		385		390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly	Thr		
	395		400		405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala	Val		
	410		415		420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr		
	425		430		435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly		
	440		445		450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp		
	455		460		465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala		
	470		475		480
Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala		
	485		490		495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg		
	500		505		510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu		
	515		520		525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg		
	530		535		540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser		
	545		550		555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala		
	560		565		570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala		
	575		580		585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
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<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggtga aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279  
gtctgttcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 280  
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
aggggtccctt agccgggagc agggcgcgca gccagggctg agatccgcgg 50  
cttcgtaga agtgagcatg gctgggcagc gaggcttct tctagtgggc 100  
ttccttctcc ctggggctct gctctcagag gctgccaaaa tcctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacgggcat aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300  
ttggccttga cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450  
ggatatcatg gattccttaa agaagagaa cttcgacatg gtgatagttg 500  
aaacttttga ctactgtcct ttctgattg ctgagaagct tgggaagcca 550  
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600  
aatccccttg tcttatgttc cagtattccg ttccttgctg actgatcaca 650  
tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700  
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
ttcacagaa ggctctaggg cagttttgtc tcattctcta ctgaaagcag 800  
agttgtggtt cattaaactct gactttgcct ttgattttgc tcgacctctg 850  
cttccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctggtt 950  
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000  
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050  
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100  
 atgtgaaaat tgtggactgg cttcctcaga gtgacctcct ggctcaccca 1150  
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200  
 catccagcat ggtgtgcccc tgggtgggat ccctctcttt ggagaccagc 1250  
 ctgaaaacat ggtccgagta gaagccaaaa agtttggtgt ttctattcag 1300  
 ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350  
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcacctgc 1400  
 gctcccaccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450  
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 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550  
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 gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700  
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 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050  
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 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150  
 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200  
 gtccctgtct ctggtgcccc cagtgaagctc cttcttggct gagcaggcat 2250  
 ggagactgta ggtttccaga tttcctgaaa aataaaaagtt tacagcgtta 2300  
 tctctcccca acctcactaa 2320

<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly



	260		265		270
Leu Met Glu Lys	Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn			
	275	280			285
Phe Ile Ala Lys	Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu			
	290	295			300
Gly Ser Met Val	Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu			
	305	310			315
Met Asn Asn Ala	Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys			
	320	325			330
Cys Gln Cys Ser	His Trp Pro Lys Asp	Val His Leu Ala Ala Asn			
	335	340			345
Val Lys Ile Val	Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His			
	350	355			360
Pro Ser Ile Arg	Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile			
	365	370			375
Met Glu Ala Ile	Gln His Gly Val Pro	Met Val Gly Ile Pro Leu			
	380	385			390
Phe Gly Asp Gln	Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys			
	395	400			405
Phe Gly Val Ser	Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu			
	410	415			420
Ala Leu Lys Met	Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser			
	425	430			435
Ala Ala Val Ala	Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser			
	440	445			450
Pro Thr Gln Arg	Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr			
	455	460			465
Gly Gly Ala Thr	His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp			
	470	475			480
His Glu Gln Tyr	Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu			
	485	490			495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala			
	500	505			510
Val Trp Trp Leu	Arg Gly Ala Arg Lys	Val Lys Glu Thr			
	515	520			

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
tgcctttgct cacctacccc aagg 24

<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggt ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50  
ggttgagggg ctgcctcttg catatgcaca cactcacaca ttctgtcaca 100  
cccgtcacac acacatacca tggttctccat cccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400  
ccaggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaagccac actggctacc 500  
 aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550  
 tgggggcccgg gtgggcccag gaggggtcag agcccgtcct gctggagggg 600  
 gagtgcctgg tggctctgtga gcctggccga gctgctgcag gggggcccgg 650  
 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700  
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750  
 ggggccatct acttcgacca ggtcctgggtg aacgagggcg gtggctttga 800  
 ccgggcctct ggctccttcg tagccctgtt ccgggggtgtc tacagcttcc 850  
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
 gacccgggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000  
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100  
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150  
 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200  
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
 gagctgtggc atctccagac caggccttcc caccaccca ccccagtta 1300  
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350  
 ggcaagggtt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400  
 ctccggttcc cccaccccag ctccctgctc aatgctgac agggacaggt 1450  
 ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttcctgtgag gaaagccagc atcacggatc 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600  
 aggctcagcc acaggcagaa ggggtgggaag ggcctggagt ctgtggctgg 1650  
 tgaggaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700  
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
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 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
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 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
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 caactagaga atggtgggtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgctact gcccttggac cctgggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 gctgtttctc tcgcgccacc actggccgcc ggcgcagct ccaggtgtcc 50  
 tagccgccca gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200  
 ccgcctactc cggggctcctg cgcggcgagc gtcaggccga ggctgaccgg 250  
 agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300  
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 catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500  
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 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650  
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 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750  
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 agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850  
 tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtgggtcgg 900  
 ggggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950  
 tgcggaaccg caagggcttt gtgaaactgg ccctgcgtca tggagctgac 1000  
 ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050  
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 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250  
 acctgtacca caccatgtac atggaggccc tgggtgaagct cttcgacaag 1300  
 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350  
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 tttgctctgt aaatttgga gtgtcatggg tgtctgtggg ttatttataa 1450  
 gaaattataa caattttgct aaacaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260										265					270				
Ala	Asp	Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr					
				275					280					285					
Lys	Gln	Val	Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln					
				290					295					300					
Lys	Lys	Phe	Gln	Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His					
				305					310					315					
Gly	Arg	Gly	Leu	Phe	Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr					
				320					325					330					
Ser	Lys	Pro	Ile	Thr	Thr	Val	Val	Gly	Glu	Pro	Ile	Thr	Ile	Pro					
				335					340					345					
Lys	Leu	Glu	His	Pro	Thr	Gln	Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr					
				350					355					360					
Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu	Phe	Asp	Lys	His	Lys	Thr					
				365					370					375					
Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu	Glu	Val	Asn							
				380					385										

<210> 293

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial

<220>



<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatcct cgaggagggc tcctggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

<400> 296  
gggcggcggg atgggggccc ggggcggcgg gcgccgcact cgctgaggcc 50  
ccgacgcagg gccggggccc gccaggggcc gaggagcgcg gcggccagag 100  
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcagggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250  
cacccgctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
gttcgtgctg cacctgctgg tcggctttgt cttcgtggcg agtggtctgg 350  
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400  
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
actggtcatg ctgctggagt ggtggtcctg cacggagtgt acactgttca 500  
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600  
gcgcttcgga gtgctgggga gctccaaggc cctcgctaag aaggagctgc 650  
tctacgtgcc cctcatcggc tggacgtggc actttctgga gattgtgttc 700  
tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggctgag 750  
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800  
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850  
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900  
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950  
atgtaaccct gaacttcaga ggaaacaaga acccgctcct gctggggatc 1000  
ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttcctct 1050  
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100  
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcattg 1150



ttgttctggtt gccaggctg gactacagtg gcacagtctt ggctcactgc 2650  
 agcctcgacc tcctgggctg cagtgatcct cccacctcag cctcccttgt 2700  
 agctgtatatt ttttgtatatt tgtattttgt agctgtagtt tttgtatatt 2750  
 ttgtggagac agcatttcac catgatgccc aggctggtct tgaactcctg 2800  
 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850  
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900  
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gccccaacta 2950  
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000  
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050  
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala
				80					85					90
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly
				95					100					105
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val
				110					115					120
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr
				125					130					135
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu
				140					145					150
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr
				155					160					165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	170	175	180
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	185	190	195
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	200	205	210
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	215	220	225
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	230	235	240
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	245	250	255
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	260	265	270
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	275	280	285
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	290	295	300
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	305	310	315
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	320	325	330
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	335	340	345
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	350	355	360
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								365		

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt ggggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

Sequence

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50

tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100

tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150

tcagtttgte ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctgggggt ctgagacctg ctccctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtcgttcct gtaatgtggg atgccatggg gtctttgcac aagcctttcc 500

tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550

atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggata 600

ctggcctgac agaatctcat cttgttttaat gctctcataa gaccacttgt 650

ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700

gttgatatggg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900  
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950  
 gcccagggtg ggcattctcta acaaactccc acgtgatgct gatgctgggc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcacttttg gaggctgagg caggctgac 1100  
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150  
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300  
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 302  
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile  
 1 5 10 15  
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe  
 20 25 30  
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly  
 35 40 45  
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val  
 50 55 60  
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp  
 65 70 75  
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr  
 80 85 90  
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln  
 95 100 105  
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu  
 110 115 120  
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr  
 125 130 135  
 Cys Gly Val Leu Leu Ser Phe Leu

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50  
 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100  
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200  
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
 ttctacccac accgtccctc cgaagcggg gacagcctca ccttgctggc 350  
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400  
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450  
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500  
 ggcgatggct cccactgccc aggcatacgc cttgctgtag tcaatcactg 550  
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600  
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650  
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700  
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750  
 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800  
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850  
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950  
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000  
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050  
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100  
 ctccctcctc tccctctgag aggcctcct atgtccctac taaagccacc 1150  
 agcaagacat agctgacagg ggctaattgg tcagtgttgg cccaggaggt 1200  
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgctccagt aagcacaggc tgcaaatcc ccaggcaaag gactgtgtgg 1300  
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350  
 agctagagct tggttcaaat gatctccaag ggcccttata cccaggaga 1400  
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450  
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500  
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
 gccaacatgg tgaaccccct gtctctacta aaaatacaaa aaaactagcc 1600  
 aggcattggt gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750  
 aattatgggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20				25					30	

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35				40					45	

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55					60	

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
				65				70					75	

Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80				85					90	

Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
				95				100					105	

Arg Arg Arg Asp

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305



CCDS: C12345.1

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 ccggtctctc gtgcccgcgc cgctggccct gggctcagcc gcactgggcg 150  
 ccgccttcgc cactggcctc ttctgtggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300  
 ggctgtctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
 caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc 400  
 gctggacctg ggcaccttca cgggtactc cggcctggcc ctggccctgg 450  
 cgctgcccgc ggacggggcg gtggtgacct gcgaggtgga cgcgagccc 500  
 ccggagctgg gacggccct gtggaggcag gccgaggcgg agcacaagat 550  
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 cgggcgaggc cggcaccttc gacgtggccg tgggtgatgc ggacaaggag 650  
 aactgctccg cctactacga gcgctgcctg cagctgctgc gaccggagg 700  
 catcctcgcc gtcctcagag tctgtggcg cgggaagggtg ctgcaacctc 750  
 cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcac 800  
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850  
 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				65					70					75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	
				80					85					90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	
				95					100					105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	
				110					115					120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	
				125					130					135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	
				140					145					150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	
				155					160					165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	
				170					175					180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	
				185					190					195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	
				200					205					210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	
				215					220					225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	
				230					235					240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	
				245					250					255	
Leu	Thr	Leu	Ala	Phe	Lys	Ile									
				260											

<210> 307  
 <211> 2272  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
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 ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200  
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

				140					145					150
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
				155					160					165
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
				170					175					180
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
				215					220					225
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
				230					235					240
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val
				260					265					270
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
				275					280					285
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
				290					295					300
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
				305					310					315
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
				365					370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
				380					385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
				395					400					405
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
				410					415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
				425					430					435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	440	445	450
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	455	460	465
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	470	475	480
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	485	490	495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	500	505	510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	515	520	525
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	530	535	540
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	545	550	555
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	560	565	570
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	575	580	585
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	590	595	600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	605	610	615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	620	625	630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	635	640	645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	650	655	660
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					665	670	

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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				20					25					30
Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45
Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60
Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile

	80		85		90
Phe Leu Leu Ser	Leu Val Asp Leu Asn	Lys Asn Phe Lys Lys	Ile		
	95	100	105		
Tyr Trp Pro Ala	Ala Lys Glu Arg Val	Glu Leu Cys Lys Leu	Ala		
	110	115	120		
Gly Lys Asp Ala	Asn Thr Glu Cys Ala	Asn Phe Ile Arg Val	Leu		
	125	130	135		
Gln Pro Tyr Asn	Lys Thr His Ile Tyr	Val Cys Gly Thr Gly	Ala		
	140	145	150		
Phe His Pro Ile	Cys Gly Tyr Ile Asp	Leu Gly Val Tyr Lys	Glu		
	155	160	165		
Asp Ile Ile Phe	Lys Leu Asp Thr His	Asn Leu Glu Ser Gly	Arg		
	170	175	180		
Leu Lys Cys Pro	Phe Asp Pro Gln Gln	Pro Phe Ala Ser Val	Met		
	185	190	195		
Thr Asp Glu Tyr	Leu Tyr Ser Gly Thr	Ala Ser Asp Phe Leu	Gly		
	200	205	210		
Lys Asp Thr Ala	Phe Thr Arg Ser Leu	Gly Pro Thr His Asp	His		
	215	220	225		
His Tyr Ile Arg	Thr Asp Ile Ser Glu	His Tyr Trp Leu Asn	Gly		
	230	235	240		
Ala Lys Phe Ile	Gly Thr Phe Phe Ile	Pro Asp Thr Tyr Asn	Pro		
	245	250	255		
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Arg Glu Ser Ser Gln	Glu		
	260	265	270		
Gly Ser Thr Ser	Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg	Val		
	275	280	285		
Cys Lys Asn Asp	Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys	Trp		
	290	295	300		
Thr Thr Phe Leu	Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly	Ser		
	305	310	315		
Asp Gly Ala Asp	Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr	Leu		
	320	325	330		
Leu Pro Thr Arg	Asp Glu Arg Asn Pro	Val Val Tyr Gly Val	Phe		
	335	340	345		
Thr Thr Thr Ser	Ser Ile Phe Lys Gly	Ser Ala Val Cys Val	Tyr		
	350	355	360		
Ser Met Ala Asp	Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala	His		
	365	370	375		

300

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	
				380					385					390	
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	
				395					400					405	
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	
				410					415					420	
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	
				425					430					435	
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	
				440					445					450	
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	
				455					460					465	
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	
				470					475					480	
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	
				485					490					495	
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	
				500					505					510	
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	
				515					520					525	
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	
				530					535					540	
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	
				545					550					555	
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	
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Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	
				575					580					585	
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	
				590					595					600	
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	
				605					610					615	
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	
				620					625					630	
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	
				635					640					645	
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	
				650					655					660	
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr	

	665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu	680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu	695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu	710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp	725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp	740	745	750
Lys His Met Gln Glu Met Lys Lys Lys Arg Asn Arg Arg His His	755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr	770	775	

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 DNA  
 Artificial  
  
 Artificial Sequence  
 1-24  
 Synthetic construct.  
 312  
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 313  
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 DNA  
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 1-45  
 Synthetic construct.

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<213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

<400> 315  
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				



	305		310		315
Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro	Gly		
	320	325	330		
Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met Ala	Pro		
	335	340	345		
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys	Ala		
	350	355	360		
Pro Asp Pro Gly	His Pro Asp Pro Leu	Thr			
	365	370			

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 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Leu Ala Ser Leu  
35 40 45

Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu  
50 55 60

Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75

Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90

Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105

Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120

Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

140	145	150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys	830		835		

<210> 318

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 319

ctgtgctctt cgggtgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

<400> 321  
cagcagtggc ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50  
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgttttgga tcttggccct aactctaatt gtctgtttt 200  
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcaactgatg 350  
gaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
gaaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650  
actttgagga ggaggagaa gatcttcact ttcctgcca cgaaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750  
gaccggtcac gccagacaag caagtgagga agaacttcca ataatgact 800  
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850  
tggtgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900  
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
tcatctgtcg tgtcatcatg ctttgtaact ggtgggtggc ccgcatgctg 1000  
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050  
atataataaa tgcattgtat tcaatgaatt tctgcctatg aggcattctg 1100  
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
tggttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322



<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
1				5					10					15	
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
 305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50  
 cagggagctg cccggctggc ctaggcagga agccgcacca tggccagcac 100  
 ggcgtgcag cttctgggct tctgctcag cttcctgggc atggtgggca 150  
 egttgatcac caccatcctg ccgactggc ggaggacagc gcacgtgggc 200  
 ccaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250  
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300  
 tggcgctgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350  
 tgcctgctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
 cacgcgctgc gccaaaggca caccgcgcaa gaccaccttt gccatcctcg 450  
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500  
 tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550  
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600  
 cgtccctctc gtcattgggt ggcaccctgc tttgcctgtc ctgccaggac 650  
 gaggcaccct acaggcccta ccaggccccg cccagggcca ccacgaccac 700  
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750  
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800  
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850  
 gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900  
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950  
 ctttagagca cagggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
 atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttgggga 1100  
 gtttggtcag tggggtttgg ttgtgatcca ggaataaacc ttgcggatgt 1150  
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50  
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100  
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150  
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200  
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
 gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350  
 tcctcctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400  
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450  
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500  
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550  
 gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600  
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650  
 gggggtgtga tgatgtgcat cgcctgccgg ggcctggcac cagaagaaac 700  
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
 aagaagatat acgatggagg tgccgcgaca gaggacgagg tacaatctta 850  
 tccttccaag cacgactatg tgtaatgctc taagacctct cagcacgggc 900  
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950  
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100  
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
 cccctcttc ctctagtca ataaacccat tgatgatcta tttccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
 ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350  
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
 agtcattttc agtttgaggc aaccaaactt ttctactgct gttgacatct 1500  
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550  
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600  
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850  
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100  
 aggtttaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15

Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75

Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80					85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
			95						100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
			110						115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
			125						130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
			140						145					150
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
			155						160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
			170						175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
			185						190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
			200						205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
			215						220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
			230						235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
			245						250					255
Ser	Lys	His	Asp	Tyr	Val									
			260											

<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50

gtagcagttc cggagtccag ctggctaaaa ctcatcccag aggataatgg 100

caacccatgc cttagaaatc gctgggctgt ttcttggtgg tggttgaatg 150

gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200

cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250

tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300

tccctgctgg ctcttttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400  
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450  
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500  
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550  
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600  
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgcgt 650  
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850  
 caaagaaact ttgatttact gttcttaact gcctaattct aattacagga 900  
 actgtgcatc agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taagggtggt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgta acatttatat ctcacataga gacatgctta 1150  
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaaggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
 atcctcttct cccagagggt ttttttttct tgtgtattaa attaacattt 1450  
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650  
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttgttc tgtgaaaaat aaatttcctt cttgtacccat ttctgttttag 1850  
 ttttactaaa atctgtaaat actgtatttt tctgttttatt ccaaatttga 1900  
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000  
 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	



Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
 tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50  
 ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100  
 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150  
 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgcaag 200  
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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
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Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
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<212> DNA

<213> Homo sapiens

<400> 331

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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

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Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
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aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

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<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met	Lys	Ile	Thr	Gly	Gly	Leu	Leu	Leu	Leu	Cys	Thr	Val	Val	Tyr
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Phe	Cys	Ser	Ser	Ser	Glu	Ala	Ala	Ser	Leu	Ser	Pro	Lys	Lys	Val
				20					25					30

Asp	Cys	Ser	Ile	Tyr	Lys	Lys	Tyr	Pro	Val	Val	Ala	Ile	Pro	Cys
				35					40					45

Pro	Ile	Thr	Tyr	Leu	Pro	Val	Cys	Gly	Ser	Asp	Tyr	Ile	Thr	Tyr
				50					55					60

Gly	Asn	Glu	Cys	His	Leu	Cys	Thr	Glu	Ser	Leu	Lys	Ser	Asn	Gly
				65					70					75

Arg	Val	Gln	Phe	Leu	His	Asp	Gly	Ser	Cys
				80					85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagt gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

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ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggttttctga 600

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<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

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Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
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<210> 337  
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gaccactgc cccagccgtc agggacccca acgcatccc agcccagcgc 250

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 <212> PRT  
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 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
 35 40 45

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Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339  
 <211> 849  
 <212> DNA  
 <213> Homo sapiens

<400> 339  
 gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50  
 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100  
 caagacccta agaaccatca gccctcagct gcacctcctc ccctccaagg 150  
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200  
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250



<210> 341  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 341  
 ccctccaagg atgacaaagg cgc 23

<210> 342  
 <211> 29  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-29  
 <223> Synthetic construct.

<400> 342  
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 343  
 atctcaggcg gcacctgtc agcc 24

<210> 344  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 344  
 gtggatgcct gcaagaaggt tggg 24

<210> 345  
 <211> 45  
 <212> DNA  
 <213> Artificial

aggacttgga tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300  
 gctttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
 tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
 gtccggagca cgggggatga acaactgggt agaattggagg ttgactgtt 550  
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600  
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700  
 ccttccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750  
 tcttggcttc ctcttactc ccatctggac ccagtcccct ggttctgtc 800  
 tggtatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agcttttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50  
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350  
aaacttccag gtggaacaag caacctatgt tctgctgcaa gcttgaagga 400  
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450  
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500  
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatgg 550  
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600  
aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650  
tcccaggatt gggactgga agctgaggat gaggggtgaag agtacagccc 700  
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750  
tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800  
ggtagggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850  
cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900  
aggagttgac cccgttcagc ctggaccac gtggcctcca ggaggcactc 950  
agtgcccgc tccccctcca gagggctctg cccgaggtgc ggcaccact 1000  
gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050  
tctgtttcca tgatgaggcc tggtcactc tctgcggac tgtacacagc 1100

atcctcgaca cagtgccag gcccttcctg aaggagatca tcctcgtgga 1150  
cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200  
ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250  
atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300  
cttcatggat gccactgcg agtgccaccc aggctggctg gagcccctcc 1350  
tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400  
gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450  
tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500  
atgtgaggaa ggcctccag tccccataa gcccacatcag gagccctgtg 1550  
gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600  
agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctcgaactgt 1650  
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cattcaaaga aaccttctac aagcatagcc cagaggcctt ctcccttgagc 1850  
aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
gggttgctcg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000  
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acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150  
gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200  
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atatatttca tgaagctgat cttttgtgt gtgtgctcct tgtgttagga 2500  
gagaaaaaag ctctatgaaa gaatatagga agttttctcct tttcacacct 2550

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.  
  
 <400> 348  
 ggagaggtgg tggccatgga cag 23  
  
 <210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 349  
 ctgtcactgc aaggagccaa cacc 24  
  
 <210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 350  
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351

cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50  
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100  
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcattcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200  
caggggaggc ccctcggccc cacgtcatgt gtgctgtgtg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcactg cacccccagc caccocatca ggctttgagg agggggccgcc 350  
ctcatcccaa tacccttggg ctatcgtgtg gggcccacc gtgtctcgag 400  
aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggt 450  
tttgacagccc ctcatgggct cgcaaccca caccacaact cagactccat 500  
gagaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
ggcattcct gttcgggggc cgtggggaag gtgtggacc ccagctctat 600  
gtcacaatta ccattccat catcattgtt ctctgggcca ctggcatcat 650  
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700  
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750  
tccccggctg gagtcaactgt gctgggggcc ttcggggact cacctacccc 800  
caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850  
acccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900  
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950  
tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000  
gcccctggcc ctccaaggg ggctggacca gtcctctctt gggaggcacc 1050  
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aactccaact ctgccctctt tggttttttc tcatgccacc ttgtctaaga 1150  
caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200  
ttctattctg gcctaccctt tggttcctga ctgtgccctt tccctcttcc 1250  
tctcaggatt cccctggtga atctgtgatg ccccaatgt tgggggtgcag 1300





Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
				20					25					30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	
Leu	Pro	Lys													

<210> 353  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
 gtttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50  
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tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350  
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
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 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120  
 Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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 gttggccggc ggcgggccc gacgggcatg gccctgctgc tgtgcctggt 100

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<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356

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Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln	125	130	135	
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140

145

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Ser Pro Arg Gly Asp Leu Pro  
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&lt;210&gt; 357

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

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<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

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Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
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Val Glu Leu

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<211> 24

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<222> 1-24

<223> Synthetic construct.

<400> 359

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<210> 360

<211> 20

<212> DNA

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<220>

<221> Artificial Sequence

<222> 1-20

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<400> 360

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<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

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<210> 362



<211> 50  
<212> DNA  
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<220>  
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<210> 364  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 364  
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 50 55 60  
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
 65 70 75  
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
 80 85 90  
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
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Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
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<400> 365  
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gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300  
catgtttata aagtaaaaaa a 1321

<210> 366  
<211> 373  
<212> PRT  
<213> Homo sapiens

<400> 366  
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Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
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Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
35 40 45  
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
50 55 60  
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
65 70 75  
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala  
 95 100 105  
 Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp  
 110 115 120  
 Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly  
 125 130 135  
 Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn  
 140 145 150  
 Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile  
 155 160 165  
 Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala  
 170 175 180  
 Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu  
 185 190 195  
 Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr  
 200 205 210  
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys  
 215 220 225  
 Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys  
 230 235 240  
 Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys  
 245 250 255  
 Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu  
 260 265 270  
 Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn  
 275 280 285  
 Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn  
 290 295 300  
 Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe  
 305 310 315  
 Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu  
 320 325 330  
 Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp  
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 Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
 365 370

<210> 367

<211> 30  
<212> DNA  
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<220>  
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<222> 1-30  
<223> Synthetic construct.

<400> 367  
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<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggtt cattctcctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
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<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
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<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
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 ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300  
 tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
 gaagctggtg gctatgtctc ctcttttgc cctgcgtgct ccctggtgga 500  
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
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 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650  
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700  
 agatggaaca ggcccagaag gccagaacc ccaggagca gaagtccttc 750  
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 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
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 tacaagcttg attgaaattc actgctcact tgatacgta ttcagaaacc 1050  
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
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Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373  
 <211> 1706  
 <212> DNA  
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<400> 373  
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 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200



ctaaaccccc tggaagggcc tgcagcaatc cctccttcc tccggtttcaa 250  
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 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350  
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aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
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Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

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Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Artificial

<400> 375  
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 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100  
 gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

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ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggtggtt ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
tttgggcggt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

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<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

```

Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
  1             5             10             15

```

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Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
          20             25             30

```

```

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
          35             40             45

```

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Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
          50             55             60

```

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Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
          65             70             75

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Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
          80             85             90

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Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcgactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50

ggcgatgtgg aggggtgcccg gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250

gggtgtctgt aggtottctc ctggtgaaaa gtgtccaggt gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatatggc atgtacacca gcaaggaccg ctattttctat 450

tttgggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggcct tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650

ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu  
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly  
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr  
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
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 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100  
 atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttctctggg 400  
 tgtcagcgag cctgactca ctacagtga gctgacagg gctgtcatgc 450  
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
 acaaaggatg gggtttcaatg taattaggct actgagcgga tcagctgtag 550  
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 cgaggatgcc ctaagggtgt taggtgtgaa ggcaaatgg tatattgtga 650



atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700  
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750  
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caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
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gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
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cgctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400  
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagtttttaa 1500  
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agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650  
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 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

	200		205		210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu	Phe		
	215	220	225		
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn	Lys		
	230	235	240		
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser	Leu		
	245	250	255		
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser	Gly		
	260	265	270		
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn	Leu		
	275	280	285		
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp	Ser		
	290	295	300		
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp	Glu		
	305	310	315		
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser	Phe		
	320	325	330		
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys	Glu		
	335	340	345		
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser	Ile		
	350	355	360		
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala	Leu		
	365	370	375		
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His	Glu		
	380	385	390		
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro	Gly		
	395	400	405		
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys	Ile		
	410	415	420		
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile	Leu		
	425	430	435		
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met	Lys		
	440	445	450		
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys	Lys		
	455	460	465		
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe	Tyr		
	470	475	480		
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu	Leu		
	485	490	495		

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 386  
 ctgggatctg aacagtttcg gggc 24

<210> 387  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 387  
 ggtccccagg acatggtctg tccc 24

<210> 388  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 388  
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
 <211> 1449  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100  
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
 ctcggaacct ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

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Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	35	40	45
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	50	55	60
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	65	70	75
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	80	85	90
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	95	100	105
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	110	115	120
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	125	130	135
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His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu	
				35					40					45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu	
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Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser	
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Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu	
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Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp	
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Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	
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Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val	
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Ser	Gly	Ser	Ile	Arg											
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Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	275	280	285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	290	295	300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	305	310	315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	320	325	330
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ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
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ccaaaaaaaa aaaaaaaaaa a 1571

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<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

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<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
 1             5             10             15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
          20             25             30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
          35             40             45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
          50             55             60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
          65             70             75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
          80             85             90

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Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
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<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

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<210> 404

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<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404  
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<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
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ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaaggag aaggctttct aaagctttgg caaggagtga 300  
cacccgccat ttacagacac gtagtgtatt ctggaggctc aatggtcaca 350  
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tccccttttg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
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<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
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1 5 10 15



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Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
			35						40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
			50						55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
			65						70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
			80						85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
			95						100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
			110						115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
			125						130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
			140						145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
			155						160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
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Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
			185						190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
			200						205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
			215						220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
			230						235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
			245						250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
			260						265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
			275						280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
			290						295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

&lt;210&gt; 407

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-31

&lt;223&gt; Synthetic construct.

&lt;400&gt; 407

cgcgatccc gttatcgtct tgcgctactg c 31

&lt;210&gt; 408

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-34

&lt;223&gt; Synthetic construct.

&lt;400&gt; 408

gcggaattct taaaatggac tgactccact catc 34

&lt;210&gt; 409

&lt;211&gt; 1487

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 409

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tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100  
cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150  
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accatgcctt tcacacatgt ggtgtattht ccacattggc thtcttcatg 350  
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380

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe  
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr  
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<210> 411  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

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<210> 412  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 412  
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<210> 413  
<211> 40  
<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

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<210> 414

<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414

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<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415

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Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

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 <212> DNA  
 <213> Artificial

<220>  
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<222> 1-21  
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 <211> 18  
 <212> DNA  
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 <222> 1-18  
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 <400> 417  
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 <210> 418  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
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 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
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 <210> 420  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
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<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
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<223> Synthetic construct.

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<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> 1528  
<223> unknown base

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<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met	Leu	Phe	Ser	Ala	Leu	Leu	Leu	Glu	Val	Ile	Trp	Ile	Leu	Ala
1				5					10					15
Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln
				20					25					30
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
				35					40					45
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
				50					55					60
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
				65					70					75
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu

80					85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala
95					100					105				
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly
110					115					120				
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His
125					130					135				
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala
140					145					150				
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu
155					160					165				
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His
170					175					180				
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro
185					190					195				
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe
200					205					210				
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val
215					220					225				
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln
230					235					240				
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro
245					250					255				
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn
260					265					270				
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr
275					280					285				
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly
290					295					300				
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile
305					310					315				
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser
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<210> 425  
<211> 18  
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<400> 425  
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<210> 426  
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<400> 426  
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<210> 427  
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<210> 428  
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gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300  
 ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350  
 gggttgaatg tacaacagca actgcaccca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
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 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
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 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
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 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
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<211> 209

<212> PRT

<213> Homo sapiens

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			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
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<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
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 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
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<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

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Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
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Leu Pro Lys

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<210> 433  
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<210> 434  
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<220>  
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<400> 434  
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<210> 435

<211> 19  
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<400> 435  
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<210> 436  
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<210> 437  
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